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<110> University of Victoria Innovation and Developement Corporation
Hintz, William E.
Eades, Caleb Joshua

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Asp Leu Leu Lys Gly Pro Ala Ala Gly Leu Val Asp Asp Ser Arg Val
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Asp Val Leu Leu Glu Gln Ser Gln Asn Leu Ala Glu Val Leu Lys Phe
145 150 155 160

Ala Phe Asp Thr Pro Ser Gly Val Pro Thr Asn Met Ile Asn Ile Thr
165 170 175

Ser Gly Gly Asn Asp Gly Ala Thr Thr Asn Gly Leu Ala Val Thr Gly
180 185 190

Thr Leu Val Leu Glu Trp Thr Arg Leu Ser Asp Leu Thr Gly Asn Asp
195 200 205

Glu Thr Ala Arg Leu Ser Gln Arg Ala Glu Asp Thr Leu Leu His Pro
210 215 220

Glu Pro Ala Gln Thr Glu Pro Phe Pro Gly Leu Ile Gly Ser Ala Val
225 230 235 240

Asn Ile Ala Asp Gly Lys Leu Ala Asn Gly His Ile Ser Trp Asn Gly
245 250 255

Gly Ala Asp Ser Thr Thr Glu Thr Leu Ile Lys Met Thr Val Thr Asp
260 265 270

Pro Glu Arg Phe Gly Leu Thr Arg Asp Arg Trp Val Ala Ala Ala Glu
275 280 285

Ser Ser Ile Asn His Leu Ala Ser His Pro Ser Thr Arg Pro Asp Val
290 295 300

Thr Phe Leu Ala Thr Thr Asn Glu Glu His Gln Leu Gly Leu Thr Ser
305 310 315 320

Gln His Leu Thr Cys Phe Asp Gly Gly Ser Phe Leu Leu Gly Gly Thr
325 330 335

Leu Leu Asp Arg Gln Asp Phe Val Asp Phe Gly Leu Asp Leu Val Ala
340 345 350

Gly Cys His Glu Thr Thr Asn Ser Thr Leu Thr Gly Ile Gly Pro Glu
355 360 365

Gln Phe Ser Trp Asp Pro Asn Gly Val Pro Asp Ser Gln Lys Glu Leu
370 375 380

Phe Glu Arg Ala Gly Phe Thr Ile Asn Ser Gly Gln Thr Ile Leu Arg
385 390 395 400

Pro Glu Val Ile Glu Ser Phe Thr Thr Ala Trp Arg Val Thr Gly Asp
405 410 415

Gly Thr Thr Leu Glu Trp Val Trp Asn Ala Phe Thr Asn Ile Asn Lys
420 425 430

Thr Cys Arg Thr Ala Thr Gly Phe Ala Gly Leu Glu Asn Val Asn Ala
435 440 445

Ala Asn Gly Gly Arg Ile Asp Asn Gln Glu Ser Phe Met Phe Ala
450 455 460

Glu Val Leu Lys Thr Ser Phe Leu Thr Phe Ala Pro Glu Asp Asp Trp
465 470 475 480

Gln Val Gln Lys Gly Ser Gly Asn Thr Phe Val Thr Asn Thr Glu Ala
485 490 495

His Pro Phe Lys Val Thr Thr Pro Gln
500 505

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<400> 7
gtaagt 6

<210> 8
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<223> n is a, c, g, or t/u

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<400> 9
gctgac 6

<210> 10
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<223> r is g or a

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rctrac 6

<210> 11
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gtacgt

6

<210> 12
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<400> 12
actgac

6

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<400> 13

Gly Gly Leu Gly Glu Ser Phe Thr Glu Thr
1 5 10

<210> 14
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<400> 14

Leu Ala Glu Thr Leu Lys Thr Leu Thr
1 5

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<223> y is t/u or c

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<221> misc_feature
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<223> y is t/u or c

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<223> n is a, c, g, or t/u

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<223> y is t/u or c

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<222> (15)..(15)
<223> r is g or a

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<222> (18)..(18)
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gggggyctng gygارتcntt ctacgagta
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29

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<220>
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<223> n is a, c, g, or t/u

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<223> n is a, c, g, or t/u

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<223> n is a, c, g, or t/u

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<222> (22)..(22)
<223> n is a, c, g, or t/u
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<221> misc_feature
<222> (25)..(25)
<223> n is a, c, g, or t/u
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<220>
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<222> (28)..(28)
<223> r is g or a
```

```
<220>
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<221> misc_feature
<222> (29)..(29)
<223> h is a, c, or t/u
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gtanaggtac tttnagngtct cngcnagrha gaa

33

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<213> Aspergillus nidulans
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Met Pro Arg Arg Trp Ser
1 5

cat agg aat aca gac aca cca cgc gcc gcc aat agg gct aca aac ggc 149
 His Arg Asn Thr Asp Thr Pro Arg Ala Ala Asn Arg Ala Thr Asn Gly
 25 30 35

```

cct gcc aac ggc ttt gct agg cag caa agc ata tgt cca tca aca ccc      197
Pro Ala Asn Gly Phe Ala Arg Gln Gln Ser Ile Cys Pro Ser Thr Pro
40          45          50

```

```

cct cag cct cca tat aac cga acc agc acg gga ggg ttc aac tgg ggt 245
Pro Gln Pro Pro Tyr Asn Arg Thr Ser Thr Gly Gly Phe Asn Trp Gly
55          60          65          70

```

gaa atc cca gtc aga tac cct gta tcc gac ttc atc ccg ctg tca acc 293
 Glu Ile Pro Val Arg Tyr Pro Val Ser Asp Phe Ile Pro Leu Ser Thr
 75 80 85

```

aac tct cct gca aca ctt ccg cgc atc caa cgc tct tcc ttc cca ctt      341
Asn Ser Pro Ala Thr Leu Pro Arg Ile Gln Arg Ser Ser Phe Pro Leu
90          95          100

```

```

caa tcc tca atc act aaa tcc cgc cag gca gca gtc aaa ggt gcc ttt      389
Gln Ser Ser Ile Thr Lys Ser Arg Gln Ala Ala Val Lys Gly Ala Phe
105          110          115

```

```

cag cgc gca tgg acc tcc tac aca acc cac gcc tgg aag gcg gac gag 437
Gln Arg Ala Trp Thr Ser Tyr Thr Thr His Ala Trp Lys Ala Asp Glu
120          125          130

```

```

gta cgg ccc atc acg gcc gga tct cga aac aac ttt ggc gga tgg gga 485
Val Arg Pro Ile Thr Ala Gly Ser Arg Asn Asn Phe Gly Gly Trp Gly
135           140           145           150

```

gcg acc cta gtc gac aat ctc gac aca ctg cta atc atg ggg ctg gac 533

Ala Thr Leu Val Asp Asn Leu Asp Thr Leu Leu Ile Met Gly Leu Asp	155	160	165		
gag gag ttc gca gca gtc gac gcg ctc gca gat ata gaa ttc agc Glu Glu Phe Ala Ala Val Asp Ala Leu Ala Asp Ile Glu Phe Ser	170	175	180	581	
ccg cac tcg tcc cca tcc tcc cag agc aca atc aac ata ttc gaa Pro His Ser Ser Pro Ser Ser Gln Ser Thr Ile Asn Ile Phe Glu	185	190	195	629	
acg aca atc cgg tat ctg ggc ggc ttg ctc gcg gcg tat gat ctc act Thr Thr Ile Arg Tyr Leu Gly Gly Leu Leu Ala Ala Tyr Asp Leu Thr	200	205	210	677	
ggc tgt cga gag act cgg ctg ctg gac aaa gca atc cag ctt ggg gag Gly Cys Arg Glu Thr Arg Leu Leu Asp Lys Ala Ile Gln Leu Gly Glu	215	220	225	230	725
atg atc tac acc tcc ttc gac aca gag aac cgc atg ccc gta cca cgg Met Ile Tyr Thr Ser Phe Asp Thr Glu Asn Arg Met Pro Val Pro Arg	235	240	245	773	
tgg aat ctg cac aaa gca ggc aac gga gag cct cag cgc gcg gca gtg Trp Asn Leu His Lys Ala Gly Asn Gly Glu Pro Gln Arg Ala Ala Val	250	255	260	821	
cag ggc gtg ctc gct gaa ctc gcc agc agc agt ctc gag ttc acg cgg Gln Gly Val Leu Ala Glu Leu Ala Ser Ser Leu Glu Phe Thr Arg	265	270	275	869	
ctg tcg cag ctg acg ggg gat atg cgg tat ttc gat gcg gca tcc cgc Leu Ser Gln Leu Thr Gly Asp Met Arg Tyr Phe Asp Ala Ala Ser Arg	280	285	290	917	
att acc gat ctg ctt gac tcc caa gcc ggc cat acc cgg atc ccg ggg Ile Thr Asp Leu Leu Asp Ser Gln Ala Gly His Thr Arg Ile Pro Gly	295	300	305	310	965
ttg tgg cca gtc agc gtg aac ctg cag aaa ggc gat ctg acc cgt ggg Leu Trp Pro Val Ser Val Asn Leu Gln Lys Gly Asp Leu Thr Arg Gly	315	320	325	1013	
tcg aca ttc agt ttt ggc ggg atg gcc gat agc gcc tac gag tat ctc Ser Thr Phe Ser Phe Gly Gly Met Ala Asp Ser Ala Tyr Glu Tyr Leu	330	335	340	1061	
ggc aag acg tat cgg ctc ctc ggt ggt gtg ggg aaa ggg cca cag tac Gly Lys Thr Tyr Arg Leu Leu Gly Gly Val Gly Lys Gly Pro Gln Tyr	345	350	355	1109	
gag cgt ctg gcg cga aac gca cta gat gcc ggg att cga cat ctc ctc Glu Arg Leu Ala Arg Asn Ala Leu Asp Ala Gly Ile Arg His Leu Leu	360	365	370	1157	
ttc cga ccg atg acg cct gat cat gca gat atc ctc cta ccc ggg gtc Phe Arg Pro Met Thr Pro Asp His Ala Asp Ile Leu Leu Pro Gly Val	375	380	385	390	1205
gcg cac gca acc agc tct tcc gtg gga ctc gag ccc cgg aca gag cat				1253	

Ala His Ala Thr Ser Ser Ser Val Gly Leu Glu Pro Arg Thr Glu His			
395	400	405	
ctc gcc tgt ttt gtg ggt ggg atg tac gcg ctc gcc ggg aag ctt ttc		1301	
Leu Ala Cys Phe Val Gly Gly Met Tyr Ala Leu Ala Gly Lys Leu Phe			
410	415	420	
tca aac cag acg tac ctc gac acc ggc cgg aag ctg aca gac ggt tgt		1349	
Ser Asn Gln Thr Tyr Leu Asp Thr Gly Arg Lys Leu Thr Asp Gly Cys			
425	430	435	
atc tgg tac tac gat aat tca ccg cta ggt atc atg ccg gag atg ttc		1397	
Ile Trp Tyr Tyr Asp Asn Ser Pro Leu Gly Ile Met Pro Glu Met Phe			
440	445	450	
acc gtg ccg gct tgt ccg tca gtg gct gaa tgt cct tgg gac gaa aca		1445	
Thr Val Pro Ala Cys Pro Ser Val Ala Glu Cys Pro Trp Asp Glu Thr			
455	460	465	470
agg ggt ggt atc tac acc tac gtg cgt gat ggg cac tac ttt ctg cgt		1493	
Arg Gly Gly Ile Tyr Thr Tyr Val Arg Asp Gly His Tyr Phe Leu Arg			
475	480	485	
cct gag gca atg gag agt atc ttc tat atg tgg cgc att aca ggg gac		1541	
Pro Glu Ala Met Glu Ser Ile Phe Tyr Met Trp Arg Ile Thr Gly Asp			
490	495	500	
gaa aag tac cgc gag gct gca tgg aga atg ttc acg gct atc gaa gcg		1589	
Glu Lys Tyr Arg Glu Ala Ala Trp Arg Met Phe Thr Ala Ile Glu Ala			
505	510	515	
gtt aca aag acg gag ttt ggg aat gcg gcg gtg cgg gat gtt atg gtt		1637	
Val Thr Lys Thr Glu Phe Gly Asn Ala Ala Val Arg Asp Val Met Val			
520	525	530	
gag gaa gga aat gta aag aga gaa gat agc atg gag agt ttc tgg atg		1685	
Glu Glu Gly Asn Val Lys Arg Glu Asp Ser Met Glu Ser Phe Trp Met			
535	540	545	550
gca gag acg ttg aag tat ctg tat ctg ata ttt ggg gag acc gat ttg		1733	
Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile Phe Gly Glu Thr Asp Leu			
555	560	565	
gtc agc ttg gac tgg gtg ttc aat acg gag gcg cac cct ttg agg		1781	
Val Ser Leu Asp Asp Trp Val Phe Asn Thr Glu Ala His Pro Leu Arg			
570	575	580	
ggt gca ggg agt tgacattgta ttcacacatc ggtatagaca aattatagag		1833	
Gly Ala Gly Ser			
585			
tagacgttca aaacggccaa aactgaatgg atagactcca tatgcattga atatacaatg		1893	
tattcgctgc aaagcatgga taaaataaag atgtacaaag tgtctttgtt gtcgctttga		1953	
aagtggata tcatccatc ataaggtggc agtgtaaacca accctctata tcacccat		2013	
agacagctga tagaccggc		2032	

<210> 18
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<400> 18

Met Pro Arg Arg Trp Ser Ser Leu Ile Ser Ile Thr Ala Ile Phe Leu
1 5 10 15

Val Leu Phe Phe Leu Leu His Arg Asn Thr Asp Thr Pro Arg Ala Ala
20 25 30

Asn Arg Ala Thr Asn Gly Pro Ala Asn Gly Phe Ala Arg Gln Gln Ser
35 40 45

Ile Cys Pro Ser Thr Pro Pro Gln Pro Pro Tyr Asn Arg Thr Ser Thr
50 55 60

Gly Gly Phe Asn Trp Gly Glu Ile Pro Val Arg Tyr Pro Val Ser Asp
65 70 75 80

Phe Ile Pro Leu Ser Thr Asn Ser Pro Ala Thr Leu Pro Arg Ile Gln
85 90 95

Arg Ser Ser Phe Pro Leu Gln Ser Ser Ile Thr Lys Ser Arg Gln Ala
100 105 110

Ala Val Lys Gly Ala Phe Gln Arg Ala Trp Thr Ser Tyr Thr Thr His
115 120 125

Ala Trp Lys Ala Asp Glu Val Arg Pro Ile Thr Ala Gly Ser Arg Asn
130 135 140

Asn Phe Gly Gly Trp Gly Ala Thr Leu Val Asp Asn Leu Asp Thr Leu
145 150 155 160

Leu Ile Met Gly Leu Asp Glu Glu Phe Ala Ala Ala Val Asp Ala Leu
165 170 175

Ala Asp Ile Glu Phe Ser Pro His Ser Ser Pro Ser Ser Gln Ser
180 185 190

Thr Ile Asn Ile Phe Glu Thr Thr Ile Arg Tyr Leu Gly Gly Leu Leu
195 200 205

Ala Ala Tyr Asp Leu Thr Gly Cys Arg Glu Thr Arg Leu Leu Asp Lys

210

215

220

Ala Ile Gln Leu Gly Glu Met Ile Tyr Thr Ser Phe Asp Thr Glu Asn
225 230 235 240

Arg Met Pro Val Pro Arg Trp Asn Leu His Lys Ala Gly Asn Gly Glu
245 250 255

Pro Gln Arg Ala Ala Val Gln Gly Val Leu Ala Glu Leu Ala Ser Ser
260 265 270

Ser Leu Glu Phe Thr Arg Leu Ser Gln Leu Thr Gly Asp Met Arg Tyr
275 280 285

Phe Asp Ala Ala Ser Arg Ile Thr Asp Leu Leu Asp Ser Gln Ala Gly
290 295 300

His Thr Arg Ile Pro Gly Leu Trp Pro Val Ser Val Asn Leu Gln Lys
305 310 315 320

Gly Asp Leu Thr Arg Gly Ser Thr Phe Ser Phe Gly Gly Met Ala Asp
325 330 335

Ser Ala Tyr Glu Tyr Leu Gly Lys Thr Tyr Arg Leu Leu Gly Val
340 345 350

Gly Lys Gly Pro Gln Tyr Glu Arg Leu Ala Arg Asn Ala Leu Asp Ala
355 360 365

Gly Ile Arg His Leu Leu Phe Arg Pro Met Thr Pro Asp His Ala Asp
370 375 380

Ile Leu Leu Pro Gly Val Ala His Ala Thr Ser Ser Val Gly Leu
385 390 395 400

Glu Pro Arg Thr Glu His Leu Ala Cys Phe Val Gly Gly Met Tyr Ala
405 410 415

Leu Ala Gly Lys Leu Phe Ser Asn Gln Thr Tyr Leu Asp Thr Gly Arg
420 425 430

Lys Leu Thr Asp Gly Cys Ile Trp Tyr Tyr Asp Asn Ser Pro Leu Gly
435 440 445

Ile Met Pro Glu Met Phe Thr Val Pro Ala Cys Pro Ser Val Ala Glu

450

455

460

Cys Pro Trp Asp Glu Thr Arg Gly Gly Ile Tyr Thr Tyr Val Arg Asp
465 470 475 480

Gly His Tyr Phe Leu Arg Pro Glu Ala Met Glu Ser Ile Phe Tyr Met
485 490 495

Trp Arg Ile Thr Gly Asp Glu Lys Tyr Arg Glu Ala Ala Trp Arg Met
500 505 510

Phe Thr Ala Ile Glu Ala Val Thr Lys Thr Glu Phe Gly Asn Ala Ala
515 520 525

Val Arg Asp Val Met Val Glu Glu Gly Asn Val Lys Arg Glu Asp Ser
530 535 540

Met Glu Ser Phe Trp Met Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile
545 550 555 560

Phe Gly Glu Thr Asp Leu Val Ser Leu Asp Asp Trp Val Phe Asn Thr
565 570 575

Glu Ala His Pro Leu Arg Gly Ala Gly Ser
580 585

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<220>
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<400> 19
rctrac

6